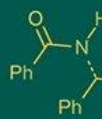


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(4): 1037-1042
www.biochemjournal.com
Received: 01-02-2026
Accepted: 04-03-2026

Pushpa Gautam
Ph.D. Scholar, Division of
Extension Education, ICAR-
Indian Veterinary Research
Institute, Izatnagar, Bareilly,
Uttar Pradesh, India

Nirbhay Bhawsar
MVSc Scholar, Division of
Extension Education, ICAR-
Indian Veterinary Research
Institute, Izatnagar, Bareilly,
Uttar Pradesh, India

Akshat Kaushik
Ph.D. Scholar, Livestock
Production and Management,
College of Veterinary Science and
Animal Husbandry, DUVASU,
Mathura, Uttar Pradesh, India

Amrita Priyadershi
Davison of Animal
Reproduction, ICAR-Indian
Veterinary Research Institute,
Izatnagar, Bareilly,
Uttar Pradesh, India

Vibha
Technical Assistant (Veterinary
Science) Lab Animal Facility,
ICMR-National Institute of
Malaria Research, Dwarka,
New Delhi, India

Khushboo Choudhary
Ph.D. Scholar, Division of
Extension Education, ICAR-
Indian Veterinary Research
Institute, Izatnagar, Bareilly,
Uttar Pradesh, India

Sonu Kumar Yadav
Assistant Professor, Department
of Livestock Production &
management, S.M. College of
Veterinary science and Animal
Research, Mathura,
Uttar Pradesh, India

Corresponding Author:
Nirbhay Bhawsar
MVSc Scholar, Division of
Extension Education, ICAR-
Indian Veterinary Research
Institute, Izatnagar, Bareilly,
Uttar Pradesh, India

Interaction between rumen microbes and host metabolism

Pushpa Gautam, Nirbhay Bhawsar, Akshat Kaushik, Amrita Priyadershi, Vibha, Khushboo Choudhary and Sonu Kumar Yadav

DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i4Sm.8280>

Abstract

Ruminant animals play an important role in livestock production, because they can convert low-quality fibrous feed into valuable products such as milk and meat. This ability is mainly due to the rumen, an anaerobic fermentation chamber that hosts diverse microorganisms, including bacteria, protozoa, fungi, archaea and bacteriophages. These microbes function symbiotically to degrade complex plant materials, produce microbial protein and generate volatile fatty acids, which serve as the primary energy source for the host. The rumen maintains stable physicochemical conditions, supporting efficient microbial growth and nutrient utilization. However, factors such as heat stress, antibiotic use, dietary changes, ruminal pH imbalance and gastrointestinal disturbances can disrupt microbial balance, reducing animal productivity. Nutritional and biotechnological approaches, including prebiotics, probiotics, enzymes and nitrogen supplements, are commonly used to restore microbial homeostasis and improve rumen function. This article provides a concise, detailed, research-based and scientific overview of rumen microorganisms and their functional roles in ruminant nutrition and productivity.

Keywords: Rumen microbiota, fibre digestion, microbial fermentation, volatile fatty acids (VFAs), ruminant nutrition

Introduction

Ruminants are vital to global livestock production because they efficiently convert low quality fibrous feeds into milk and animal protein through the unique structure of their stomach especially the rumen which functions as a fermentation chamber. This organ hosts a complex anaerobic microbial community including bacteria protozoa and fungi that ferment feed and produce volatile fatty acids and microbial protein which serve as primary energy and nutrient sources for the host animal (Van Soest 1994 McDonald *et al.* 2011) [42, 25]. The symbiotic association between microbes and the host enables digestion of fibre rich diets and utilization of non protein nitrogen while microbial enzymes degrade plant structural carbohydrates such as cellulose to release usable energy (Hungate 1966 Russell & Rychlik 2001) [17, 1]. Moreover ruminal microbes synthesize B complex vitamins and certain amino acids thereby reducing the need for dietary supplementation and supporting growth productivity and health (Flint *et al.* 2008 Wallace *et al.* 2019) [9, 44]. With increasing demand for animal derived foods current research focuses on biotechnological manipulation of the rumen ecosystem to improve feed efficiency animal health and overall production performance (Patra & Yu 2015) [35].

Function of the Rumen Microbial Ecosystem

Ruminant animals mainly consume plant structural carbohydrates such as cellulose, hemicellulose and lignin, but they are unable to digest these compounds directly due to the absence of endogenous fibrolytic enzymes. Consequently, they depend on a symbiotic population of microorganisms present in the rumen that produce cellulolytic and hemicellulolytic enzymes capable of degrading complex plant polymers (Van Soest, 1994) [42]. Through microbial fermentation, these substrates are converted into volatile fatty acids (VFAs), microbial protein and gases, which provide a major portion of the energy requirements for the host animal while also supporting microbial growth and activity (Hungate, 1966; Russell and Rychlik, 2001) [17, 1].

The rumen functions as a highly anaerobic environment characterized by a low redox potential and relatively constant temperature, conditions that support the predominance of obligate anaerobic microorganisms along with a limited number of facultative anaerobes (Stewart *et al.*, 1997) ^[40]. The rumen microbial ecosystem is generally divided into three major domains: Bacteria, Archaea and Eucarya (Whitman *et al.*, 1998) ^[45]. Bacteria represent the most abundant group and are primarily responsible for fiber degradation, carbohydrate fermentation and protein metabolism (Flint *et al.*, 2008) ^[9]. Archaea, mainly methanogenic species, utilize hydrogen and carbon dioxide produced during fermentation to form methane, thereby maintaining hydrogen balance within the rumen environment (Hook *et al.*, 2010) ^[16]. The Eucarya domain includes protozoa and anaerobic fungi, which contribute to starch digestion, breakdown of fibrous plant materials and stabilization of rumen fermentation (Orpin and Joblin, 1997; Williams and Coleman, 1992) ^[32, 46]. Together, these microbial populations interact synergistically to enhance nutrient digestibility, improve feed utilization efficiency and support the health and productivity of ruminant animals (Mackie *et al.*, 2000) ^[24].

Table 1: Distribution of Rumen Microbial Population (per g rumen content)

Microorganism	Population
Bacteria	10 ¹⁰ -10 ¹¹ (>200 species)
Ciliate protozoa	10 ⁵ -10 ⁶ (25 genera)
Archaea	10 ⁷ -10 ⁸
Anaerobic fungi	10 ³ -10 ⁵ (6 genera)
Bacteriophages	10 ⁸ -10 ⁹

Table 2: Physical Properties

Parameter	Typical Range
Dry matter (%)	10-18%
Temperature	38-41 °C
pH	5.5-6.9 (average around 6.4)
Redox potential	-350 to -400 mV
Osmolality	250-350 mOsmol/kg

Table 3: Chemical Properties

Parameter	Description
Amino acids	Continuously present in rumen fluid
Ammonia	Ranges between 2-12 mmol/L
Dietary fibre components	Includes cellulose, pectin, and hemicellulose
Soluble carbohydrates	Present and available for microbial fermentation
Lactate	Usually maintained below 1 mmol/L (2-3 hours after feeding)
Non-volatile acids	Less than 1 mmol/L (2-3 hours post-feeding)
Volatile fatty acids	Acetate (60-90%), Propionate (15-30%), Butyrate (10-25%)
Growth factors	Include branched-chain fatty acids, purines, and pyrimidines
Trace elements and vitamins	Adequate supply available in rumen
Vitamin supply	Vitamin B-complex synthesized and present
Minerals	High sodium concentration with overall good mineral availability
Gas phase composition (%)	CO ₂ (65%), CH ₄ (27%), N ₂ (7%), O ₂ (0.6%), H ₂ (0.2%)

Table-1, 2, 3 [Source: Adapted from Van Soest (1994) ^[42]; Hungate (1966) ^[17]; Hobson & Stewart (1997) ^[40]; Mackie *et al.* (2000) ^[24]]

Diversity of Rumen Microorganisms

- Bacteria:** Bacteria are the most abundant microorganisms in the rumen and are mainly strict anaerobes forming over ninety five percent of the microbial population (Hungate 1966 Russell and Rychlik 2001) ^[17, 1]. They are classified as solid associated liquid associated and epimural bacteria based on their location. Solid associated bacteria dominate fiber digestion whereas liquid associated bacteria utilize soluble nutrients in rumen fluid. Epimural bacteria are attached to the rumen wall and help maintain anaerobic conditions. Rumen bacteria also vary by substrate use including cellulose hemicellulose pectin starch and amino acids. Cellulose is degraded mainly by *Fibrobacter succinogenes* *Ruminococcus albus* and *Ruminococcus flavefaciens* while starch fermentation is carried out by *Streptococcus bovis* *Selenomonas ruminantium* and *Ruminobacter amylophilus* (Flint *et al.* 2008 McDonald *et al.* 2011) ^[9, 25]. Amino acids are utilized especially by *Prevotella* species supporting microbial growth and energy production (Wallace *et al.* 2019) ^[44].
- Protozoa:** Protozoa are fewer in number within the rumen microbial population yet they contribute nearly fifty percent of the total microbial biomass and most belong to ciliate groups while flagellates are less common. These organisms are strict anaerobes that depend on the host animal for nutrient supply and play an important role in ruminal digestion with estimates suggesting that they contribute up to sixty two percent of cellulolytic activity (Hungate 1966) ^[17]. Protozoa engulf bacteria and feed particles and digest carbohydrates, proteins and lipids thereby influencing nutrient turnover within the rumen. Maintaining an appropriate protozoal population is essential for sustaining a balanced rumen environment and supporting efficient functioning of other microbial groups. Protozoa also regulate fermentation by moderating rapid substrate degradation by other microorganisms which helps prevent excessive lactic acid production and reduces lactate accumulation thus minimizing the risk of a decline in ruminal pH (Williams and Coleman 1992, Wallace *et al.* 2019) ^[46, 44].
- Archaea:** *Methanogenic archaea* are regarded as among the earliest forms of life on Earth and they represent an important component of the rumen microbial ecosystem. These microorganisms utilize hydrogen and carbon dioxide produced during fermentation by bacteria protozoa and fungi to generate energy in the form of adenosine triphosphate. Methanogens commonly exist in close symbiotic association with rumen microbes particularly ciliate protozoa and this relationship enhances methane formation within the rumen (Hungate 1966) ^[17]. The interaction between methanogens and protozoa has been reported to contribute substantially to total methane emissions with estimates indicating that protozoa associated methanogens may account for nearly thirty seven percent of ruminal methane

production (Morgavi *et al.* 2010) ^[26]. The population dynamics of *Methanogenic archaea* are influenced by factors such as diet composition feeding level and feeding frequency and alterations in these conditions modify rumen fermentation patterns which ultimately affect methane output (Patra and Yu 2015) ^[35].

- **Fungi:** Rumen fungi account for approximately five to twenty percent of the total microbial biomass and produce a wide range of enzymes such as cellulase xylanase and other hydrolases that are essential for plant fiber degradation. These fungi survive under strictly anaerobic conditions of the rumen and differ from most other fungi because they possess hydrogenosomes instead of mitochondria which enables them to generate hydrogen as a metabolic product that is utilized by methanogenic archaea (Bauchop and Mountfort 1981) ^[1]. Rumen fungi play a crucial role in the breakdown of fibrous plant components as their strong enzymatic system allows efficient degradation of complex plant structural materials often giving them an advantage in fiber colonization compared to bacteria. Through this activity they significantly enhance the digestion of low-quality roughages and improve nutrient availability to the host animal (Orpin 1988) ^[31].
- **Bacteriophages:** Bacteriophages form an important component of the rumen microbial ecosystem and function as obligate parasites of bacteria by infecting and lysing bacterial cells. This lytic activity contributes to the continuous turnover of bacterial biomass in the rumen which may not always be beneficial depending on feeding conditions and rumen stability (Hobson and Stewart 1997) ^[40]. The breakdown of bacterial cells releases intracellular proteins that can become a source of amino acids for the host animal thereby contributing indirectly to nutrient supply. In addition, bacteriophages and their associated lytic enzymes influence rumen microbial ecology by regulating bacterial populations including those involved in methanogenesis and thereby affecting overall fermentation patterns and microbial balance.

Factors Responsible for Microbial Dysbiosis

- **Physiological disturbances:** Stress can significantly alter rumen microbial populations mainly by reducing feed intake and affecting metabolism immunity physiology and behavior of the animal. Heat stress in particular induces marked shifts in ruminal fermentation leading to decreased ruminal pH and acetate concentration along with increased lactate levels (West 2003) ^[47]. This condition is also associated with changes in microbial composition including an increase in some cellulolytic groups such as Fibrobacteres due to their relatively higher heat tolerance. In contrast acetate producing bacteria including Actinobacteria and Acetobacter generally decline under heat stress conditions which further disrupts normal fermentation patterns. These physiological and microbial adjustments collectively influence rumen fermentation as well as blood biochemical and metabolic profiles of the animal (Collier *et al.* 2012) ^[7].
- **Oral Antibiotics:** A balanced gastrointestinal microbiota is essential for maintaining the health and productivity of ruminant animals. However, antibiotics are widely used in livestock to treat infections such as

respiratory diseases and bacterial diarrhea. Although they are effective against pathogens, they also disrupt beneficial microbial populations leading to disturbance of normal microbial equilibrium. In recent years concerns have increased regarding their adverse effects including the development of antimicrobial resistance and alterations in host associated microbiota. A major consequence of antibiotic use is microbial dysbiosis which is associated with impaired host metabolism immune dysfunction and increased susceptibility to disease. Antibiotics can also suppress gastrointestinal fermentation by inhibiting microbial growth and reducing functional diversity of rumen microbes (Jernberg *et al.* 2010) ^[19]. Their administration alters both rumen fluid and mucosal microbial communities and recovery of the microbiota after treatment may require a prolonged period. This disruption can further reduce volatile fatty acid production and impair microbial protein synthesis thereby negatively affecting overall rumen efficiency and animal performance (Gresse *et al.* 2019) ^[14].

- **Feed Modifications:** Rumen microorganisms are broadly classified into fibre degrading microbes attached to the rumen mat and rapidly growing microbes suspended in rumen fluid that utilize sugars and starch (Hungate 1966 Russell and Rychlik 2001) ^[17]. Their population and activity depend mainly on diet as feed composition determines substrate availability. Concentrate rich and young forage diets promote rapid fermentation and faster passage rate while high fibre mature forages support slower digestion and reduce intake (Van Soest 1994) ^[42]. Legumes enhance microbial activity due to higher protein and minerals whereas poor quality roughages like rice straw reduce cellulolytic bacteria and fermentation efficiency (McDonald *et al.* 2011) ^[25]. Urea treatment of crop residues improves nitrogen availability and restores microbial growth leading to better rumen fermentation (Patra *et al.* 1996) ^[35].
- **Ruminal pH Alterations:** High producing dairy cows often experience disturbed homeostasis because feeding systems are aimed at maximizing milk yield and this increases the risk of metabolic disorders. Ruminal acidosis is one of the most common conditions and is mainly associated with high concentrate feeding to meet the elevated energy demand for milk production (Nocek 1997) ^[29]. Changes in ruminal fermentation occur as rumen microflora and ruminal papillae adapt to dietary shifts while volatile fatty acid production plays a key role in regulating ruminal pH. Microbial activity in the rumen is highly sensitive to pH fluctuations and acidic conditions suppress microbial growth by disrupting intracellular hydrogen ion balance (Russell and Rychlik 2001) ^[1]. The transition period from late pregnancy to early lactation is particularly critical because major metabolic changes occur and ruminal pH often drops to around 5.2 to 5.6 which increases the risk of subacute ruminal acidosis (Plaizier *et al.* 2008) ^[36].
- **Gastrointestinal Hypermotility:** Ruminal motility and contractions are essential for maintaining normal digestive function in farm animals. Rumen protozoa can alter their movement behavior in response to changes in diet and physiological conditions, reflecting adaptations within the rumen environment (Hungate 1966) ^[17].

During diarrhoeic conditions animals suffer loss of fluids and nutrients along with a reduction in beneficial rumen microflora which can disturb fermentation and digestion processes. Restoration of the normal microbial population is therefore important for reestablishing rumen function and maintaining digestive efficiency and overall health (Russell and Rychlik 2001) ^[1].

Re-establishment of Gut Microbial Homeostasis

Prebiotics: A prebiotic is a non-digestible dietary component that selectively stimulates the growth and activity of beneficial intestinal bacteria thereby improving host health (Gibson and Roberfroid 1995) ^[11]. Common prebiotics such as fructooligosaccharides, galactooligosaccharides, xylooligosaccharides, isomaltoligosaccharides and lactulose promote populations of lactobacilli and other beneficial microbes while suppressing pathogens through competitive exclusion for binding sites and nutrients in the gut environment. These compounds help reduce the risk of intestinal infections and support microbial balance by shaping the gut microbiota composition. Prebiotics can also modulate immune responses indirectly through microbial fermentation and stimulation of beneficial bacterial growth. In addition, supplementation has been associated with improved growth performance and feed efficiency in calves including better average daily gain and feed conversion ratio (Ohashi and Ushida 2009) ^[30]. Furthermore, prebiotics enhance the production of short chain fatty acids particularly butyrate which serves as an important energy source for colonocytes and supports intestinal mucosal integrity and gut health (Slavin 2013).

Enzymes: Cellulose and hemicellulose are the main structural components of plant cell walls and are naturally insoluble, but they can be broken down into simpler sugars by fibrolytic enzymes that are utilized by rumen microbes for energy production (Van Soest 1994) ^[42]. The use of fibrolytic enzyme supplements in ruminant diets enhances feed efficiency by improving the breakdown of forage in the rumen, which increases dry matter digestibility and voluntary feed intake (Beauchemin *et al.* 2003) ^[2]. This better fibre degradation also improves the availability of total digestible nutrients and modifies volatile fatty acid production patterns, ultimately supporting improved growth and productivity. These enzyme preparations are commonly produced from fungi such as *Trichoderma longibrachiatum*, *Aspergillus niger*, *Penicillium funiculosum*, and *Aspergillus oryzae*, as well as bacterial sources like *Bacillus* spp. (Kong *et al.* 2015) ^[22]. Originally developed for silage and roughage treatment, they are now widely used as feed additives to improve rumen fermentation and nutrient utilization efficiency.

Probiotics: Probiotics are defined as live microorganisms or components of microbial cells that have beneficial effects on host, since they regulate intestinal flora to improve animal health. Probiotics used in ruminant feed mainly include bacteria, fungi and yeast, which have replaced conventional antibiotics as growth promoters. Specific strains of microorganisms are used to improve animal health and productivity in animal feed

Lactobacillus sporogenes: *Lactobacillus sporogenes* supports the growth of lactic acid utilizing bacteria which helps reduce lactic acid accumulation in the rumen and lowers ruminal acidity thereby stabilizing rumen pH (Fuller 1989) ^[10]. By regulating lactic acid levels, it also helps reduce the risk of enteric infections caused by pathogens such as *E. coli* and *Salmonella* species (FAO/WHO 2002). Probiotic bacteria including *Lactobacillus* and *Bifidobacterium* have shown beneficial effects in ruminants by improving growth performance feed efficiency and overall health status through better microbial balance and fermentation efficiency (Ouweland *et al.* 2002) ^[33].

Saccharomyces cerevisiae: *Saccharomyces cerevisiae* supplementation in ruminants has been shown to improve dry matter intake, enhance nutrient digestibility, and maintain a more stable ruminal pH (Newbold *et al.* 1996) ^[28]. It supports rumen fermentation by stimulating hydrogen-utilizing acetogenic bacteria, which helps reduce methane formation and improves overall fermentation efficiency, while also increasing the production of beneficial volatile fatty acids such as propionate and butyrate that contribute to better energy supply and fibre utilization. The yeast also functions as an oxygen scavenger by removing residual oxygen from the rumen environment, thereby encouraging strict anaerobic conditions, promoting lactate-utilizing bacteria, and suppressing lactate-producing microbes, which helps in maintaining rumen stability and preventing acid accumulation. Additionally, it lowers rumen redox potential, which favours the attachment and activity of cellulolytic bacteria on feed particles and enhances cellulose breakdown (Chaucheyras-Durand and Fonty 2001) ^[3]. Overall, it supports the growth of key fibrolytic bacteria such as *Fibrobacter succinogenes* and *Ruminococcus albus*, leading to improved fibre digestion, better nutrient availability, and enhanced animal performance (Poppy *et al.* 2012) ^[37].

Aspergillus oryzae: *Aspergillus oryzae* produces fibrolytic enzymes like cellulases and hemicellulases that improve fibre breakdown and utilization in the rumen (Beauchemin *et al.* 2003) ^[2]. Its supplementation in dairy cows enhances feed intake, nutrient utilization, and rumen stability. It also reduces pH drop after feeding, increases volatile fatty acid production, and lowers lactic acid accumulation (Morgavi *et al.* 2000) ^[26]. Overall, fungal probiotics such as *Aspergillus oryzae*, *Saccharomyces cerevisiae*, and *Candida* improve milk yield, feed efficiency, and animal performance (Fuller 1989) ^[10].

Nitrogenous Supplements: Supplementation of non-protein nitrogen sources such as urea is commonly used to meet nitrogen requirements in ruminants but its effectiveness can be limited when animals consume low quality forages with low natural protein content (Van Soest 1994) ^[42]. In contrast additional crude protein improves fibre digestion by stimulating the growth of cellulolytic rumen bacteria and enhancing overall fermentation efficiency. Protein supplementation in animals grazing poor quality forage has been shown to improve body weight gain and reduce grazing time due to better nutrient availability and microbial activity in the rumen (Klopfenstein *et al.* 2001). This ultimately results in improved feed utilization and productivity in ruminants.

Conclusion

The rumen microbial ecosystem is a complex and dynamic community of bacteria protozoa fungi archaea and bacteriophages that collectively drive fermentation of fibrous feeds and production of volatile fatty acids microbial protein and essential nutrients for the host animal. Stable rumen microbial balance is critical for optimal animal performance but can be disturbed by stress antibiotic use sudden dietary changes and ruminal pH fluctuations leading to dysbiosis reduced feed efficiency and poor productivity. Nutritional and biotechnological interventions such as prebiotics probiotics exogenous enzymes and nitrogen supplementation help restore microbial balance improve fibre degradation and stabilize rumen fermentation. These strategies enhance nutrient utilization promote beneficial microbes and support better growth milk production and feed conversion efficiency while also contributing to more sustainable ruminant production systems.

References

- Bauchop T, Mountfort DO. Cellulose fermentation by a rumen anaerobic fungus in the presence of methanogens. *Appl Environ Microbiol.* 1981;42(1):110-116.
- Beauchemin KA, Colombatto D, Morgavi DP, Yang WZ. Use of exogenous fibrolytic enzymes to improve feed utilization by ruminants. *J Anim Sci.* 2003;81(Suppl 2):E37-E47.
- Chaucheyras-Durand F, Fonty G. Establishment of cellulolytic bacteria and development of ruminal hydrogenotrophy in gnotobiotically reared lambs. *Appl Environ Microbiol.* 2001;67(12):5320-5327.
- Chaucheyras-Durand F, Ossa F. The rumen microbiome: composition, abundance, diversity, and new investigative tools. *Prof Anim Sci.* 2014;30(1):1-12.
- Chaucheyras-Durand F, Walker ND, Bach A. Effects of active dry yeast on rumen microbial ecosystem. *Anim Feed Sci Technol.* 2008;145(1-4):5-26.
- Church DC. The ruminant animal: digestive physiology and nutrition. Waveland Press; 1993.
- Collier RJ, Bauman DE, McGuire MA, Baumgard LH. Metabolic and physiological responses to heat stress in dairy cattle. *J Dairy Sci.* 2012;95(12):6512-6525.
- FAO/WHO. Guidelines for the evaluation of probiotics in food. Food Agric Organ/World Health Organ; 2002.
- Flint HJ, Bayer EA, Rincon MT, Lamed R, White BA. Polysaccharide utilization by gut bacteria: potential for new insights from genomic analysis. *Nat Rev Microbiol.* 2008;6(2):121-131.
- Fuller R. Probiotics in man and animals. *J Appl Bacteriol.* 1989;66(5):365-378.
- Gibson GR, Roberfroid MB. Dietary modulation of the human colonic microbiota: introducing the concept of prebiotics. *J Nutr.* 1995;125(6):1401-1412.
- Gibson GR, Hutkins R, Sanders ME, Prescott SL, Reimer RA, Salminen SJ, *et al.* Expert consensus on the definition of prebiotics. *Nat Rev Gastroenterol Hepatol.* 2017;14(8):491-502.
- Gressley TF. Zinc, copper, manganese, and selenium in dairy cattle nutrition. *Vet Clin North Am Food Anim Pract.* 2010;26(2):325-341.
- Gresse R, Chaucheyras-Durand F, Fleury MA, van de Wiele T, Forano E, Blanquet-Diot S. Gut microbiota dysbiosis and recovery. *Microorganisms.* 2019;7(6):163.
- Hobson PN, Stewart CS. The rumen microbial ecosystem. 2nd ed. Blackie Acad Prof; 1997.
- Hook SE, Wright ADG, McBride BW. Methanogens: methane producers of the rumen and mitigation strategies. *Appl Environ Microbiol.* 2010;76(21):713-720.
- Hungate RE. The rumen and its microbes. Academic Press; 1966.
- Jami E, White BA, Mizrahi I. Potential role of the rumen microbiome in modulating animal productivity. *Appl Environ Microbiol.* 2013;79(10):3166-3175.
- Jernberg C, Lofmark S, Edlund C, Jansson JK. Long-term impacts of antibiotic exposure on human intestinal microbiota. *ISME J.* 2010;4(5):569-578.
- Kadzere CT, Murphy MR, Silanikove N, Maltz E. Heat stress in lactating dairy cows. *Livest Prod Sci.* 2002;77(1):59-91.
- Klopfenstein TJ, Erickson GE, Berger LL. NPN usage in ruminants. *J Anim Sci.* 2001;79(Suppl):E153-E161.
- Kong Y, *et al.* Effects of fibrolytic enzymes on rumen fermentation and feed digestibility. *Anim Feed Sci Technol.* 2015;208:1-12.
- Krause DO, Nagaraja TG, Wright ADG, Callaway TR. Rumen microbiology: leading the way in microbial ecology. *J Anim Sci.* 2013;91(1):331-341.
- Mackie RI, White BA, Isaacson RE. Gastrointestinal microbiology. Springer; 2000.
- McDonald P, Edwards RA, Greenhalgh JFD, Morgan CA, Sinclair LA, Wilkinson RG. Animal nutrition. 7th ed. Pearson; 2011.
- Morgavi DP, Beauchemin KA, Nsereko VL, Rode LM, Iwaasa AD, Yang WZ, *et al.* Synergy between ruminal fibrolytic enzymes and microorganisms. *J Dairy Sci.* 2000;83(6):1310-1321.
- Nagaraja TG, Titgemeyer EC. Ruminal acidosis in beef cattle. *J Anim Sci.* 2007;85:E17-E22.
- Newbold CJ, Wallace RJ, McIntosh FM. Mode of action of *Saccharomyces cerevisiae* as a feed additive for ruminants. *Br J Nutr.* 1996;76(2):249-261.
- Nocek JE. Bovine acidosis: implications on laminitis. *J Dairy Sci.* 1997;80(5):1005-1028.
- Ohashi Y, Ushida K. Health-beneficial effects of probiotics. *Anim Sci J.* 2009;80(1):1-8.
- Orpin CG. The role of anaerobic fungi in rumen fibre degradation. *Biosystems.* 1988;21(4):403-414.
- Orpin CG, Joblin KN. The rumen anaerobic fungi. In: Hobson PN, Stewart CS, editors. The rumen microbial ecosystem. 2nd ed. Blackie Acad Prof; 1997. p.140-195.
- Ouwehand AC, Salminen S, Isolauri E. Probiotics: an overview. 2002.
- Patra AK, Saxena J. A new perspective on the use of probiotics in ruminant nutrition. *Vet World.* 2010;3(4):193-198.
- Patra AK, Yu Z. Effects of dietary manipulation on rumen microbiome and methane emission: a review. *Anim Nutr.* 2015;1(2):69-78.
- Plaizier JC, Krause DO, Gozho GN, McBride BW. Subacute ruminal acidosis in dairy cows. *J Dairy Sci.* 2008;91(4):1177-1195.
- Poppy GD, Rabiee AR, Lean IJ, Sanchez WK, Dorton KL. Effects of yeast culture on dairy cattle performance. *J Dairy Sci.* 2012;95(10):5865-5876.

38. Russell JB, Rychlik JL. Factors that alter rumen microbial ecology. *Science*. 2001;292(5519):1119-1122.
39. Slavin J. Fiber and prebiotics: mechanisms and health benefits. *Nutrients*. 2013;5(4):1417-1435.
40. Stewart CS, Flint HJ, Bryant MP. *The rumen bacteria*. Springer; 1997.
41. Tricarico JM, Johnston JD, Dawson KA. Dietary supplementation with *Aspergillus oryzae*. *J Anim Sci*. 2008;86:E134-E144.
42. Van Soest PJ. *Nutritional ecology of the ruminant*. 2nd ed. Cornell Univ Press; 1994.
43. Wallace RJ, Newbold CJ, McIntosh FM. Role of yeast culture in rumen fermentation. *J Anim Sci*. 2002;80:E24-E32.
44. Wallace RJ, Rooke JA, McKain N, Duthie CA, Hyslop JJ, Ross DW, *et al*. The rumen microbial metagenome associated with high methane production in cattle. *BMC Genomics*. 2019;16:839.
45. Whitman WB, Coleman DC, Wiebe WJ. Prokaryotes: the unseen majority. *Proc Natl Acad Sci USA*. 1998;95(12):6578-6582.
46. Williams AG, Coleman GS. *The rumen protozoa*. Springer; 1992.
47. West JW. Effects of heat stress on production in dairy cattle. *J Dairy Sci*. 2003;86(6):2131-2144.